

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/566,054
Source: IFWP
Date Processed by STIC: 02/07/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/10/566,054

TIME: 13:53:23

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Output Set: N:\CRF4\02012006\J566054.raw

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3 <110> APPLICANT: Ambrose, Helen Jean
4   March, Ruth
6 <120> TITLE OF INVENTION: USE OF POLYMORPHISMS IN HUMAN OATP-C ASSOCIATED WITH AN
EFFECT ON STATIN
7   PHARMACOKINETICS IN HUMANS IN STATIN THERAPY
9 <130> FILE REFERENCE: 06275-492US1
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/566,054
C--> 11 <141> CURRENT FILING DATE: 2006-01-25
11 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/003236
12 <151> PRIOR FILING DATE: 2004-07-26
14 <150> PRIOR APPLICATION NUMBER: GB 0317592.4
15 <151> PRIOR FILING DATE: 2003-07-26
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 691
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo Sapiens
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33          20          25          30
36 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
37          35          40          45
40 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
41          50          55          60
44 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
45 65          70          75          80
48 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
49          85          90          95
52 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
53          100         105         110
56 Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
57          115         120         125
60 Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
61          130         135         140
64 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
65 145         150         155         160
68 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
69          165         170         175
72 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
73          180         185         190
76 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr

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80 Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
81          210          215          220
84 Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
85 225          230          235          240
88 Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
89          245          250          255
92 Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
93          260          265          270
96 Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
97          275          280          285
100 Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
101          290          295          300
104 Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
105 305          310          315          320
108 Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
109          325          330          335
112 Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
113          340          345          350
116 Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
117          355          360          365
120 Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
121          370          375          380
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129          405          410          415
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133          420          425          430
136 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
137          435          440          445
140 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
141          450          455          460
144 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
145 465          470          475          480
148 Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
149          485          490          495
152 Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
153          500          505          510
156 Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
157          515          520          525
160 Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
161          530          535          540
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165 545          550          555          560
168 Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser
169          565          570          575
172 Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly
173          580          585          590

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176 Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly
 177 595 600 605
 180 Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val
 181 610 615 620
 184 Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr
 185 625 630 635 640
 188 Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile
 189 645 650 655
 192 Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser
 193 660 665 670
 196 Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu
 197 675 680 685
 200 Thr His Cys
 201 690

204 <210> SEQ ID NO: 2

205 <211> LENGTH: 2050

206 <212> TYPE: DNA

207 <213> ORGANISM: Homo Sapiens

209 <400> SEQUENCE: 2

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 212 tgcaaatatc atacaattaa tctaattagg tgttgaatct ataatgtgcc aggcattatg 120
 214 taaggcactt tacatacact aaatctttat tccaaatata gacttcttac tttatagatg 180
 216 agtgcactga tgctcagaaa tggtaaataa cctactgatg tttatactgc tggcaggtag 240
 218 cagagacata tcggcattta agtctttcag acttcaaagg ccatgatatt tcatcagagc 300
 220 tgtgatagcc gttcctgaaa aaaatatcag ctgattcttt aaatcaattt ttgtcatcta 360
 222 actgatgcgt ggctgttagc ataattattga tcttgaaaga tgttttgcaa catctttccc 420
 224 ctgggtgact cttgtttttc catgatccca caaaatgagc agtctaatta tttacacaat 480
 226 taggaagaga aaagggggcac agagaatgct ctttgacctc tgaaaatatt ggagaatttt 540
 228 acaactggca cctttagctc aggattataa aggttggttag ttagtttgta ctgttttacc 600
 230 ttcattgtat ataatatata tattagtctc caaacatggt gatgtgtttt caatgaaatg 660
 232 gatgtctgag gagaaaaacca ttagcctgag aaaacccaaa ctgtattccc attgtgaata 720
 234 aaaggaagtc cataaaaaatg atggaaaatg ttctgcattc ctgttatgat atcaaaatct 780
 236 ggcagtacat gaaaattttt caaagtgcct atttaacagg cataatcttt ggtctcctga 840
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 242 gttctgcaca gtcattcttc cctctacac tactctttag tttgtctcat gattccaata 1020
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 264 aagcaagag ggtatatttt aattttttaa tgccaatgta acctgtaggc atatttttta 1680
 266 tttgtcttaa attatttcct atttggaagt tttaaatacc tggaataatt tattgtactc 1740
 268 atatttttaa agaaaaaaat cttatgccac caacttaatt gaataaacia gtaaaagcca 1800

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274 tttgactaga gcaatgacat aataaggtgg ttaatcatca ctggacttgt tttcaaaaag 1980
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291 tctatatttc aatcatggac caaatcaaac atttgaataa aacagcagag gcacaacctt 180
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307 agatagtggg aaaaggttgt ttaaaggaat ctgggtcata catgtggata tatgtgttca 660
309 tgggtaatat gcttcgtgga ataggggaga ctcccatagt accattgggg ctttcttaca 720
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319 tctttttctt gccccaaact ccaaataaac cacaaaaaga aagaaaagct tcaactgtct 1020
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349 caatggttat acgagcacta ggaggaattc tagctccaat atattttggg gctctgattg 1920
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361 aaagccactt ctgcttctgt gtttccaaac agcattgcac tgattcagta agatgttatt 2280
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367 ttacattata gctacatatt tgtgggtaag gttagactat atgatccata caaattaaag 2460
369 tgagagacat gggtactgtg taataaaaga aaaaatactt gttcaggtaa ttctaattct 2520
371 taataaaaca aatgagtatc atacaggtag aggttaaaaa ggaggagcta gattcatatc 2580
373 ctaagtaaag agaaatgcct agtgtctatt ttattaaaca aacaaacaca gagtttgaac 2640
375 tataatacta aggcctgaag tctagcttgg atatatgcta caataatatc tgttactcac 2700
377 ataaaattat atatttcaca gactttatca atgtataatt aacaattatc ttgtttaagt 2760
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385 <211> LENGTH: 691
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo Sapiens
389 <400> SEQUENCE: 4
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399 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
400 35 40 45
403 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
404 50 55 60
407 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
408 65 70 75 80
411 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
412 85 90 95
415 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
416 100 105 110
419 Leu Pro His Phe Phe Met Gly Tyr Arg Tyr Ser Lys Glu Thr Asn
420 115 120 125
423 Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
424 130 135 140
427 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
428 145 150 155 160
431 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Ala Phe Met
432 165 170 175
435 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
436 180 185 190
439 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
440 195 200 205
443 Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
444 210 215 220
447 Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
448 225 230 235 240
451 Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
452 245 250 255
455 Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
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459 Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys

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RAW SEQUENCE LISTING ERROR SUMMARY

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date